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RAW SEQUENCE LISTING

DATE: 02/19/2003

PATENT APPLICATION: US/09/888,035A

TIME: 14:36:30

Input Set : A:\SPO-115C1.ST25.txt

Output Set: N:\CRF4\02192003\I888035A.raw

3 <110> APPLICANT: Fukuda, Atsunori
 4 Tanaka, Yoshiyuki
 6 <120> TITLE OF INVENTION: Sodium/Proton Antiporter Gene
 8 <130> FILE REFERENCE: SPO-115C1
 10 <140> CURRENT APPLICATION NUMBER: 09/888,035A
 11 <141> CURRENT FILING DATE: 2001-06-22
 13 <150> PRIOR APPLICATION NUMBER: JP 1998-365604
 14 <151> PRIOR FILING DATE: 1998-12-22
 16 <160> NUMBER OF SEQ ID NOS: 2
 18 <170> SOFTWARE: PatentIn version 3.1
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 2330
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Oryza sativa
 25 <220> FEATURE:
 26 <221> NAME/KEY: CDS
 27 <222> LOCATION: (297)..(1901)
 28 <223> OTHER INFORMATION:

ENTERED

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 34 accaaatccc gattttctcaa cctgaatccc cccccacgt tcctcgtttc aatctgttcg 120
 36 tctgcgaatc gaattctttg tttttttttc tctaatttta ccggaattg tcgaattagg 180
 38 cattcaccaa cgagcaagag gggagtggat tggttggtta aagctccgca tcttgcgcg 240
 40 gaaatctcgc tctcttctct gcggtgggtg gccggagaag tcgccgccg tgaggc atg 299
 41 Met
 42 1
 44 ggg atg gag gtg gcg gcg gcg cgg ctg ggg gct ctg tac acg acc tcc 347
 45 Gly Met Glu Val Ala Ala Ala Arg Leu Gly Ala Leu Tyr Thr Thr Ser
 46 5 10 15
 48 gac tac gcg tcg gtg gtg tcc atc aac ctg ttc gtc gcg ctg ctc tgc 395
 49 Asp Tyr Ala Ser Val Val Ser Ile Asn Leu Phe Val Ala Leu Leu Cys
 50 20 25 30
 52 gcc tgc atc gtc ctc ggc cac ctc ctc gag gag aat cgc tgg gtc aat 443
 53 Ala Cys Ile Val Leu Gly His Leu Leu Glu Glu Asn Arg Trp Val Asn
 54 35 40 45
 56 gag tcc atc acc gcg ctc atc atc ggg ctc tgc acc ggc gtg gtg atc 491
 57 Glu Ser Ile Thr Ala Leu Ile Ile Gly Leu Cys Thr Gly Val Val Ile
 58 50 55 60 65
 60 ttg ctg atg acc aaa ggg aag agc tcg cac tta ttc gtc ttc agt gag 539
 61 Leu Leu Met Thr Lys Gly Lys Ser Ser His Leu Phe Val Phe Ser Glu
 62 70 75 80
 64 gat ctc ttc ttc atc tac ctc ctc cct ccg atc atc ttc aat gca ggt 587
 65 Asp Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn Ala Gly

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66	85	90	95	
68 ttt cag gta aag aaa aag caa ttc ttc cgg aat ttc atg acg atc aca				635
69 Phe Gln Val Lys Lys Lys Gln Phe Phe Arg Asn Phe Met Thr Ile Thr				
70	100	105	110	
72 tta ttt gga gcc gtc ggg aca atg ata tcc ttt ttc aca ata tct att				683
73 Leu Phe Gly Ala Val Gly Thr Met Ile Ser Phe Phe Thr Ile Ser Ile				
74	115	120	125	
76 gct gcc att gca ata ttc agc aga atg aac att gga acg ctg gat gta				731
77 Ala Ala Ile Ala Ile Phe Ser Arg Met Asn Ile Gly Thr Leu Asp Val				
78 130	135	140	145	
80 gga gat ttt ctt gca att gga gcc atc ttt tct gcg aca gat tct gtc				779
81 Gly Asp Phe Leu Ala Ile Gly Ala Ile Phe Ser Ala Thr Asp Ser Val				
82	150	155	160	
84 tgc aca ttg cag gtc ctc aat cag gat gag aca ccc ttt ttg tac agt				827
85 Cys Thr Leu Gln Val Leu Asn Gln Asp Glu Thr Pro Phe Leu Tyr Ser				
86	165	170	175	
88 ctg gta ttc ggt gaa ggt gtt gtg aac gat gct aca tca att gtg ctt				875
89 Leu Val Phe Gly Glu Gly Val Val Asn Asp Ala Thr Ser Ile Val Leu				
90	180	185	190	
92 ttc aac gca cta cag aac ttt gat ctt gtc cac ata gat gcg gct gtc				923
93 Phe Asn Ala Leu Gln Asn Phe Asp Leu Val His Ile Asp Ala Ala Val				
94	195	200	205	
96 gtt ctg aaa ttc ttg ggg aac ttc ttt tat tta ttt ttg tcg agc acc				971
97 Val Leu Lys Phe Leu Gly Asn Phe Phe Tyr Leu Phe Leu Ser Ser Thr				
98 210	215	220	225	
100 ttc ctt gga gta ttt gct gga ttg ctc agt gca tac ata atc aag aag				1019
101 Phe Leu Gly Val Phe Ala Gly Leu Leu Ser Ala Tyr Ile Ile Lys Lys				
102	230	235	240	
104 cta tac att gga agg cat tct act gac cgt gag gtt gcc ctt atg atg				1067
105 Leu Tyr Ile Gly Arg His Ser Thr Asp Arg Glu Val Ala Leu Met Met				
106	245	250	255	
108 ctc atg gct tac ctt tca tat atg ctg gct gag ttg cta gat ttg agc				1115
109 Leu Met Ala Tyr Leu Ser Tyr Met Leu Ala Glu Leu Leu Asp Leu Ser				
110	260	265	270	
112 ggc att ctc acc gta ttc ttc tgt ggt att gta atg tca cat tac act				1163
113 Gly Ile Leu Thr Val Phe Phe Cys Gly Ile Val Met Ser His Tyr Thr				
114	275	280	285	
116 tgg cat aac gtc aca gag agt tca aga gtt aca aca aag cac gca ttt				1211
117 Trp His Asn Val Thr Glu Ser Ser Arg Val Thr Thr Lys His Ala Phe				
118 290	295	300	305	
120 gca act ctg tcc ttc att gct gag act ttt ctc ttc ctg tat gtt ggg				1259
121 Ala Thr Leu Ser Phe Ile Ala Glu Thr Phe Leu Phe Leu Tyr Val Gly				
122	310	315	320	
124 atg gat gca ttg gat att gaa aaa tgg gag ttt gcc agt gac aga cct				1307
125 Met Asp Ala Leu Asp Ile Glu Lys Trp Glu Phe Ala Ser Asp Arg Pro				
126	325	330	335	
128 ggc aaa tcc att ggg ata agc tca att ttg cta gga ttg gtt ctg att				1355
129 Gly Lys Ser Ile Gly Ile Ser Ser Ile Leu Leu Gly Leu Val Leu Ile				
130	340	345	350	

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134      355      360      365
136 aag aag gca ccg aat gaa aaa ata acc tgg aga cag caa gtt gta ata      1451
137 Lys Lys Ala Pro Asn Glu Lys Ile Thr Trp Arg Gln Gln Val Val Ile
138 370      375      380      385
140 tgg tgg gct ggg ctg atg aga gga gct gtg tgc att gct ctt gct tac      1499
141 Trp Trp Ala Gly Leu Met Arg Gly Ala Val Ser Ile Ala Leu Ala Tyr
142      390      395      400
144 aat aag ttt aca aga tct ggc cat act cag ctg cac ggc aat gca ata      1547
145 Asn Lys Phe Thr Arg Ser Gly His Thr Gln Leu His Gly Asn Ala Ile
146      405      410      415
148 atg atc acc agc acc atc act gtc gtt ctt ttt agc act atg gta ttt      1595
149 Met Ile Thr Ser Thr Ile Thr Val Val Leu Phe Ser Thr Met Val Phe
150      420      425      430
152 ggg atg atg aca aag cca ttg atc agg ctg ctg cta ccg gcc tca ggc      1643
153 Gly Met Met Thr Lys Pro Leu Ile Arg Leu Leu Leu Pro Ala Ser Gly
154      435      440      445
156 cat cct gtc acc tct gag cct tca tca cca aag tcc ctg cat tct cct      1691
157 His Pro Val Thr Ser Glu Pro Ser Ser Pro Lys Ser Leu His Ser Pro
158 450      455      460      465
160 ctc ctg aca agc atg caa ggt tct gac ctc gag agt aca acc aac att      1739
161 Leu Leu Thr Ser Met Gln Gly Ser Asp Leu Glu Ser Thr Thr Asn Ile
162      470      475      480
164 gtg agg cct tcc agc ctc cgg atg ctc ctc acc aag ccg acc cac act      1787
165 Val Arg Pro Ser Ser Leu Arg Met Leu Leu Thr Lys Pro Thr His Thr
166      485      490      495
168 gtc cac tac tac tgg cgc aag ttc gac gac gcg ctg atg cga ccg atg      1835
169 Val His Tyr Tyr Trp Arg Lys Phe Asp Asp Ala Leu Met Arg Pro Met
170      500      505      510
172 ttt ggc ggg cgc ggg ttc gtg ccc ttc tcc cct gga tca cca acc gag      1883
173 Phe Gly Gly Arg Gly Phe Val Pro Phe Ser Pro Gly Ser Pro Thr Glu
174      515      520      525
176 cag agc cat gga gga aga tgaacagtgc aaagaaatga gaatggaatg      1931
177 Gln Ser His Gly Gly Arg
178 530      535
180 gttgatgagg agaatacatg taaaatgtga cagcaaaaga gagaaggcaa gttttggggt      1991
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184 atggtgcctc accaaggcct aagagccagg aggaccttct gataatgggt cgggatgatt      2111
186 ggtttgttct gtcaggatga accctagtga gtgacacagg gtgatgtgct ccgacaacct      2171
188 gtaaaatttg tagattaaca gccccatttg tacctgtcta ccatctttag ttggcgggtg      2231
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203 1          5          10          15
206 Ser Asp Tyr Ala Ser Val Val Ser Ile Asn Leu Phe Val Ala Leu Leu
207          20          25          30
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211          35          40          45
214 Asn Glu Ser Ile Thr Ala Leu Ile Ile Gly Leu Cys Thr Gly Val Val
215          50          55          60
218 Ile Leu Leu Met Thr Lys Gly Lys Ser Ser His Leu Phe Val Phe Ser
219 65          70          75          80
222 Glu Asp Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn Ala
223          85          90          95
226 Gly Phe Gln Val Lys Lys Lys Gln Phe Phe Arg Asn Phe Met Thr Ile
227          100          105          110
230 Thr Leu Phe Gly Ala Val Gly Thr Met Ile Ser Phe Phe Thr Ile Ser
231          115          120          125
234 Ile Ala Ala Ile Ala Ile Phe Ser Arg Met Asn Ile Gly Thr Leu Asp
235          130          135          140
238 Val Gly Asp Phe Leu Ala Ile Gly Ala Ile Phe Ser Ala Thr Asp Ser
239 145          150          155          160
242 Val Cys Thr Leu Gln Val Leu Asn Gln Asp Glu Thr Pro Phe Leu Tyr
243          165          170          175
246 Ser Leu Val Phe Gly Glu Gly Val Val Asn Asp Ala Thr Ser Ile Val
247          180          185          190
250 Leu Phe Asn Ala Leu Gln Asn Phe Asp Leu Val His Ile Asp Ala Ala
251          195          200          205
254 Val Val Leu Lys Phe Leu Gly Asn Phe Phe Tyr Leu Phe Leu Ser Ser
255          210          215          220
258 Thr Phe Leu Gly Val Phe Ala Gly Leu Leu Ser Ala Tyr Ile Ile Lys
259 225          230          235          240
262 Lys Leu Tyr Ile Gly Arg His Ser Thr Asp Arg Glu Val Ala Leu Met
263          245          250          255
266 Met Leu Met Ala Tyr Leu Ser Tyr Met Leu Ala Glu Leu Leu Asp Leu
267          260          265          270
270 Ser Gly Ile Leu Thr Val Phe Phe Cys Gly Ile Val Met Ser His Tyr
271          275          280          285
274 Thr Trp His Asn Val Thr Glu Ser Ser Arg Val Thr Thr Lys His Ala
275          290          295          300
278 Phe Ala Thr Leu Ser Phe Ile Ala Glu Thr Phe Leu Phe Leu Tyr Val
279 305          310          315          320
282 Gly Met Asp Ala Leu Asp Ile Glu Lys Trp Glu Phe Ala Ser Asp Arg
283          325          330          335
286 Pro Gly Lys Ser Ile Gly Ile Ser Ser Ile Leu Leu Gly Leu Val Leu
287          340          345          350
290 Ile Gly Arg Ala Ala Phe Val Phe Pro Leu Ser Phe Leu Ser Asn Leu
291          355          360          365
294 Thr Lys Lys Ala Pro Asn Glu Lys Ile Thr Trp Arg Gln Gln Val Val
295          370          375          380
298 Ile Trp Trp Ala Gly Leu Met Arg Gly Ala Val Ser Ile Ala Leu Ala
299 385          390          395          400

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302 Tyr Asn Lys Phe Thr Arg Ser Gly His Thr Gln Leu His Gly Asn Ala
303                               405                410                415
306 Ile Met Ile Thr Ser Thr Ile Thr Val Val Leu Phe Ser Thr Met Val
307                               420                425                430
310 Phe Gly Met Met Thr Lys Pro Leu Ile Arg Leu Leu Leu Pro Ala Ser
311                               435                440                445
314 Gly His Pro Val Thr Ser Glu Pro Ser Ser Pro Lys Ser Leu His Ser
315                               450                455                460
318 Pro Leu Leu Thr Ser Met Gln Gly Ser Asp Leu Glu Ser Thr Thr Asn
319 465                               470                475                480
322 Ile Val Arg Pro Ser Ser Leu Arg Met Leu Leu Thr Lys Pro Thr His
323                               485                490                495
326 Thr Val His Tyr Tyr Trp Arg Lys Phe Asp Asp Ala Leu Met Arg Pro
327                               500                505                510
330 Met Phe Gly Gly Arg Gly Phe Val Pro Phe Ser Pro Gly Ser Pro Thr
331                               515                520                525
334 Glu Gln Ser His Gly Gly Arg
335                               530                535

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VERIFICATION SUMMARY

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